

1 GAACCACCA GAAGGAAGAA ACTCCAAACA CATCCGAACA TCAGAACGGAG CAAACTCGTG ACACGCCACC TTTAAGAACCC GTGACACTCA AGCCTAGGGT
 CTTGGGTTGT CTTCTTCTTCT TGAGCTTGT GTAGCTTCTC GTTGCAGCAC TGTGCCTGG AAATCTTGG CACTGTGAGT TGGCATCCCA
 101 CGCGGGTTTC ATTCTTGAAG TCAGTGAGAC CAAGAACCCA CCAATTCCCG ACACGGAAA GTAACATCCCT AGAC ATG GCT TTA GAG ATC CAC
 GGCGCCGAAG TAAGAACCTTC AGTCACCTTG GTTCTTGGGT GGTTAAGGCC TGTGCCTGGT CATTGTAGGA TCTG TAC CGA AAT CTC TAG GTG
 1 M A L E I H
 193 ATG TCA GAC CCC ATG TGC CTC ATC GAG AAC TTT AAT GAG CAG CTG AAG GTT AAT CAG GAA GCT TTG GAG ATC CTG TCT GCC
 TAC AGT CTG GGG TAC ACG GAG TAG CTC TTG AAA TTA CTC GTC GAC TTC CAA TTA GTC CTT CGA AAC CTC TAG GAC AGA CGG
 7 M S D P M C L I E N F N E Q L K V N Q E A L E I L S A
 274 ATT ACG CAA CCT GTG GTT GTG GTA GCG ATT GTG GGC CTC TAT CGC ACT GGC AAA TCC TAC CTG ATG AAC AAG CTG GCT GGG
 TAA TGC GTT GGA CAT CAA CAC CAT CGC TAA CAC CGC GAG ATA GCG TGA CCG TTT AGG ATG GAC TAC TTG TTC GAC CGA CCC
 34 I T Q P V V V V A I V G L Y R T G K S Y L M N K L A G
 355 AAG AAC AAG GGC TTC TCT GTT GCA TCT ACC GTG CAG TCT CAC ACC AAG GGA ATT TGG ATA TGG TGT GTG CCT CAT CCC AAC
 TTC TTG TCC CCG AAG AGA CAA CGT AGA TGC CAC GTC AGA GTG TGG TTC CCT TAA ACC TAT ACC ACA CAC GGA GTA GGG TGG
 61 K N K G F S V A S T V Q S H T K G I W I W C V P H P N
 436 TGG CCA AAT CAC ACA TTA GTT CTG CTT GAC ACC GAG GGC CTG GGA GAT GTA CAG AAG GCT GAC AAC AAG AAT GAT ATC CAG
 ACC GGT TTA GTG TGT AAT CAA GAC GAA CTG TGG CTC CCG GAC CCT CTA CAT CTC TTC CGA CTG TTG TTC TTA CTA CTA TAG GTC
 88 W P N H T L V L L D T E G L G D V E K A D N K N D I Q
 517 ATC TTT GCA CTG GCA CTC TTA CTG AGC AGC ACC TTT GTG TAC AAT ACT GTG AAC AAA ATT GAT CAG GGT GCT ATC GAC CTA
 TAG AAA CGT GAC CGT GAG AAT GAC TCG TCG TGG AAA AAC CAC ATG TTA TGA CAC CCT TTG TTT TAA CTA CTC GTC CCA CGA TAG CTG GAT
 115 I F A L A L L L S S T F V Y N T V N K I D Q G A I D L
 598 CTG CAC AAT GTG ACA GAA CTC ACA GAT CTG CTC AAC GCA AGA AAC TCA CCC GAC CTT GAC AGG GTT GAA GAT CCT GCT GAC
 GAC GTG TTA CAC TGT CTT GAC TGT CTA GAC GAG TTC CGT TCT TTG AGT GGG TCC CAA CCT CTA CGA CGA CTG
 142 L H N V T E L T D L L K A R N S P D L D R V E D P A D
 679 TCT GCG AGC TTC TTC CCA GAC TTA GTG TGG ACT CTG AGA GAT TTC TGC TTA GGC CTG GAA ATA GAT GGG CAA CCT GTC ACA
 AGA CGC TCG AAG AAG GGT CTC AAT CAC ACC TGA GAC TCT CTA AAG ACG AAT CCG GAC CCT TAT CTA CCC GTT GAA CAG TGT
 169 S A S F F P D L V W T L R D F C L G L E I D G Q L V T
 760 CCA GAT GAA TAC CTG GAG AAT TCC CTA AGG CCA AAG CAA GGT AGT GAT CAA AGA GTT CAA AAT TTC AAT TTG CCC CGT CTG
 GGT CTA CTT ATG GAC CTC TTA AGG GAT TCC GGT TTC GTT CCA TCA CTA GTT TCT CAA GTT TTA AAG TTA AAC GGG GCA GAC
 196 P D E Y L E N S L R P K Q G S D Q R V Q N P N L P R L
 841 TGT ATA CAG AAG TTC TTT CCA AAA AAG AAA TGC TTT ATC TTT GAC TTA CCT GCT CAC CAA AAA AAG CTT GCC CAA CCTT GAA
 ACA TAT GTC TTC AAG AAA GGT TTT TTC TTT AGC AAA TAG AAA CTG AAT GCA CGA GTG GTT TTT TCT GAA CGG GTT GAA CCTT
 223 C I Q K F F P K K K C F I F D L P A H Q K K L A Q L E
 922 ACA CTG CCT GAT GAT GAG CTA GAG CCT GAA TTT GTG CAA CAA GTG ACA GAA TTC TGT TCC TAC ATC TTT AGC CAT TCT ATG
 TGT GAC GGA CTA CTC GAT CTC GGA CTT AAA AAC GTT CTT CAC TGT CTT AAG ACA AGG ATG TAG AAA TCG GTA AGA TAC
 250 T L P D D E L E P E F V Q Q V T E F C S Y I F S H S M
 1003 ACC AAG ACT CTT CCA GGT GGC ATC ATG GTC AAT GGA TCT CGT CTA AAG AAC CTG GTG CTG ACC TAT GTC AAT GCC ATC AGC
 TGG TTC TGA GAA GGT CCA CCG TAG TAC CAG TTA CCT AGA GCA GAT TTC TTG GAC CAC GAC TGG ATA CAG TTA CGG TAG TCG
 277 T K T L P G G I M V N G S R L K N L V L T Y V N A I S
 1084 ACT GGG GAT CTG CCT TGC ATA GAG AAT GCA GTC CTG GCC TTG GCT CAG AGA GAG AAC TCA GCT GCA GTG CAA AAG GCC ATT
 TCA CCC CTA GAC GGA ACG TAT CTC TTA CGT CAG GAC CGG AAC CGA GTC TCT CTC TTG AGT CGA CGT CAC GTT TTC CGG TAA
 304 S G D L P C I E N A V L A L A Q R E N S A A V Q K A I
 1165 GCC CAC TAT GAC CAG CAA ATG GGC CAG AAA GTG CAG CTG CCC ATG GAA ACC CTC CAG CTG CTG GAC CGT CAC AGG ACC
 CGG GTG ATA CTG GTC GTT TAC CGC GTC TTT CAC GTC GAC CGG TAC CTT TTG GAG GTC CTC GAC GAC CTG GAC GTG TCC TGG
 331 A H Y D Q Q M G Q K V Q L P M E T L Q E L L D L H R T
 1246 AGT GAG AGG GAG GCC ATT GAA GTC TTC ATG AAA AAC TCT TTC AAG GAT GTC GAC CAA AGT TTC CAG AAA GAA TTG GAG ACT
 TCA CTC TCC CTC CGG TAA CTT CAG AAG TAC TTT TTG AGA AAG TTC CTA CAT CTG GTT TCA AAG GTC TTT CTT ACC CTC TCA
 358 S E R E A I E V F M K N S F K D V D Q S F Q K E L E T
 1327 CTA CTA GAT GCA AAA CAG AAT GAC ATT TGT AAA CGG AAC CTG GAA GCA TCC TCG GAT TAT TGC TCG GCT TTA CTT AAG GAT
 GAT GAT CTA CGT TTT GTC TTA CTG TAA ACA TTT GCC TTG GAC CTT CGT AGG AGC CTA ATA AGC CGA AAT GAA TTC CTA
 385 L L D A K Q N D I C K R N L E A S S D Y C S A L L K D
 1408 ATT TTT GGT CCT CTA GAA GAA GCA GTG AAG CAG GGA ATT TAT TCT AAG CCA CGA GGC CAT ATT CTC TTC ATT CAG AAA ACA
 TAA AAA CCA CGA GAT CTT CTT CGT CAC TTC GTC CCT TAA ATA AGA TTC GTC CGA CTT CCT CAA GAC GTC TTT ATA AAT TTC AGG
 412 I F G P L E E A V K Q G I Y S K P G G H N L F I Q K T
 1489 GAA GAA CTG AAG GCA AAG TAC TAT CGG GAG CCT CGG AAA GGA ATA CAG GCT GAA GAA GTT CTG CAG AAA TAT TTA AAG TCC
 CTT CTT GAC TTC CGT TTC ATG ATA GCC CTC GGA GCC TTT CCT TAT GTC CGA CTT CCT CAA GAC GTC TTT ATA AAT TTC AGG
 439 E E L K A K Y Y R E P R K G I Q A E E V L Q K Y L K S
 1570 AAG GAG TCT GTG AGT CAT GCA ATA TTA CAG ACT GAC CAG GCT CTC ACA GAG AGC GCG GAA AAA AAG AGG AAA GAG GCA CAA GTG
 TTC CTC AGA CAC TCA GTA CGT TAT AAT GTC TGA CTG GTC CGA GAG TGT CTC TGC CTT TTT TTC TCT TTT CTC CGT GTT CAC
 466 K E S V S H A I L Q T D Q A L T E T E K K K E A Q V
 1651 AAA GCA GAA GCT GAA AAG GCT GAA GCG CAA AGG TTG GCG GCG ATT CAA AGG CAG AAC GAG CAA ATG ATG CAG GAG AGG GAG
 TTT CGT CTT CGA CTT TTC CGA CTT CGC GTT TCC AAC CGC CGC TAA GTT TCC CTC TTG CTC GTT TAC TAC GTC CTC TCC CTC
 493 K A E A E K A E Q O R L A A I Q R Q N E Q M M Q E R E
 1732 AGA CTC CAT CAG GAA CAA GTG AGA CAA ATG GAG ATA GCC AAA CAA AAT TGG CTG GCA GAG CAA CAG AAA ATG CAG GAA CAA
 TCT GAG GTA GTC CTT GTT CAC TCT GTT TAC CTC TAT CGG TTT GTT TTA ACC GAC CGT CTC GTT GTC TTT TAC GTC CTT GTT
 520 R L H Q E Q V R Q M E I A K Q N W L A E Q Q K M Q E Q
 1813 CAG ATG CAG GTA TTC ATC AAT TGT TTC ATC TCT CCC CTG CCT GTC AGC ATG AGA GTC GAA GAG CTC TGT AGC AGT GGC AAA GAG GGA GAG
 GTC TAC GTC CAT AAG TAG TTA ACA AAG TAG AGA GGG GAC GGA CAT TGC TAC TCT CAT ACA TCG TCA CGG TTT CTC CCT CTC
 547 Q M Q V F I N C F I S P L P V T M R V C S S G K E G E
 1894 GCA GCA AGA TCT TGT GGC TCT CAG CAG GGA GTC TGG AGC CAG AAA GTC TGG GTC GAA GAG CTC TGT ATCCAAGCTC CACCTCTAG TAAGTATATG
 CGT CGT TCT AGA ACA CGG AGA GCA CGC GTC CCT CAG ACC TCG GTC TTT CAG ACC CAT ACT TAGGTTCCAG CTGGAGAAC ATTCAATAC
 574 A A R S C G S Q Q G V W S Q K V W V V O
 1981 GTTGTAGGCAA GTTATCTATC ACCTCTGTG CTAATTTCC TCCC
 CAAATCCGTT CAATAGATAG TGGAGACACG GATTTAAAGG AGGC

FIG. 1

GBP - 1	1	MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTG
GBP - 2	1	MAPEINLPGPMSSLIDNTKGOLVNVPEALKILSAITQPVVVVAIVGLYRTG
GBP - 4	1	MALEIHMSDPMCLIENFNEQLKVNQEALEEILSAITQPVVVVAIVGLYRTG
GBP - 1	51	KSYLMNKLAKKKGFLGSLGTVQSHTKGIWMMWCVPHPKPGHILVLLDTEG
GBP - 2	51	KSYLMNKLAKKKNGFSLGTVKSHTKGIWMMWCVPHPKPEHTLVLLDTEG
GBP - 4	51	KSYLMNKLAKKNKGFSVASTVQSHTKGIWIVCVPHPNWPNTLVLLDTEG
GBP - 1	101	LGDVEKGDNQNSWIFALAVLLSSTFVYNSIGTINQQAMDQLYVTELTH
GBP - 2	101	LGDIEKGDNENDSWIFALAILLSSTFVYNSMGTINQQAMDQLHYVTELTD
GBP - 4	101	LGDVEKADNKNDIQIFALALLLSSTFVYNTVNKIDQGAIIDLHNVTELTD
GBP - 1	151	RIRSKSSPDENEENEVEDSADFVSFFPDFVWTLRDFSLDLEADGQPLTPDE
GBP - 2	151	RIKANSSPG--NNNSVDDSDADFVSFFPAFVWTLRDFTLELEVGDGEPIТАDD
GBP - 4	151	LLKARNSPD--LDRVEDPADSASFFPDLVWTLRDFCLGLEIDGQLVTPDE
GBP - 1	201	YLTYSLKLKKGTSQLDETFLNPLRLCIRKFFPKKCFVFDRLPVHRRKLAQL
GBP - 2	199	YLELSSLKLRKGTDKKSFSFNDPRLCIRKFFPKRKCFVFDWPAPKKYLAHL
GBP - 4	199	YLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKCFIFDLPAHQKKLAQL
GBP - 1	251	EKLQDEELDPEFVQQVADFCSYIFSNNSKTKTLSGGIQVNGPRLESLVLTY
GBP - 2	249	EQLKEEELNPDFIEQVAEFCSYILSHSNVKTLSGGIAVNGPRLESLVLTY
GBP - 4	249	ETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLY
GBP - 1	301	VNAISSLPCMCENAVLALAQIENSAVQKAIAYEQQMGQKVQLPTESL
GBP - 2	299	VNAISSLPCMCENAVLALAQIENSAVEKAIAHYEQQMGQKVQLPTETL
GBP - 4	299	VNAISSLPCMCENAVLALAQRENSAAVQKAIAYDQQMGQKVQLPTEML
GBP - 1	351	QELLDLHRDSEREAIEVFIRSFKVDHLFQKELAAQLEKKRDDFKQNO
GBP - 2	349	QELLDLHRDSEREAIEVFMKNSFKVDQMFQRKLGQLEARRDDFKQNS
GBP - 4	349	QELLDLHRDSEREAIEVFMKNSFKVDQSFQKELETLLDAKQNDTICKRN
GBP - 1	401	EASSDRCSGLLQVIFSPLLEEVKAGIYSKPGGYRLFVQKLQDLKKKYYE
GBP - 2	399	KASSDCMALLQDIFGPLEEDVKQGTFSKPGGYRLFTQKLQELKNKYYQV
GBP - 4	399	EASSDYCSALLKDIIFGPLEEAVKQGIYSKPGGHNLFIQKTEELKAKYYRE
GBP - 1	451	PRKGIAQAEELQTYLKSKESTMIDAILQTDQTLTEKEKEIEVERVKAESAQ
GBP - 2	449	PRKGIAQAKEVLKKYLESKEDVADALLQTDQSLSEKEKAIEVERIKAESAЕ
GBP - 3	1	-----ECVKAESAQ
GBP - 4	449	PRKGIAQAEELQYLKSKEVSHAILQTDQALTETEKKKKEAQVKAEEAK
GBP - 1	501	ASAKMLOEMQRKNEQMMEQKERSYQEHLKQLTEKMENDRVQLLKEQERTL
GBP - 2	499	AАКМЛЕЕИОКНЕЕММЕQKEKSYQEHVKQLTEKMERDRAQLMAEQEKTЛ
GBP - 3	10	ASAKMVEEMQIKYQOMMEEKEKSYQEHVKQLTEKMENDRVQLLKEQERTL
GBP - 4	499	AEAQRLLAAIQRQNEQMMQERERLHQEQVРQMEIAKQNWLAЕQQKMQEQQM
GBP - 1	551	ALKLQEQQEQLLKEGFQKESRIMKNEIQDLOLTKMRRKA-CTIS
GBP - 2	549	ALKLQEQQERLLKEGFENESKRLQKDIWDIQMRSKSLEPICNIL
GBP - 3	60	ALKLQ-----****
GBP - 4	549	QVFINCFIGSPUPVTMRVCSSGKEGEAARSCGSQQGVWSQKVWV

FIG. 2

mouse.purine.nuc.BP	1	- - - - - MEAPICLIVENWKNQLTVNLEAIRILEQIAQPLVVVAIVGL
mu.GBP1	1	- MASEI - - HMSEPMCLIENTEAQLVINQEAIRILSAITQPVVVVAIVGL
rat.GBP.p67	1	MDMASEI - - HMLQPMCLIENTEAHLVINQEAIRILSAINQPVVVVAIVGL
pig.GBP-1.partial	1	- NFHGIWSTTMDPIXILVKNQNNHLTVNPKALKILGEICQPVVVVIAAGL
pig.GBP-1.NH2.term.	1	- MASKV - - HMPEPQCLIENTINGRLAVNPKALKILSAIKQPLVVVAIVGL
chicken.GBP	1	- MDTPV - - LMPAPPLRLVTNKDGVLALNTAALAVLRSVTQPVVVVAIAGP
GBP-4	1	- MALEI - - HMSDPMCLIFNEQLKVNQEALEILSAITQPVVVVAIVGL
mouse.purine.nuc.BP	41	YRTGKSYLMNRLAGRNHGFSLGSTVQSETKGIWMWCVPHPKPTKPTHTLVLL
mu.GBP1	47	YRTGKSYLMNKLAKGRTGFSLGSTVQSHTKGIWMWCVPHPKPKAGQTLVLL
rat.GBP.p67	49	YRTGKSYLMNKLAKGRTGFSLGSTVQSHTKGIWMWCVPHPKPKAGQTLVLL
pig.GBP-1.partial	49	YRTGKSYLMNRLAGQNHGFRLGSTVRSSETKGIXMWCVPHPXKXDHILVLL
pig.GBP-1.NH2.term.	47	YRTGKSYLMNKLAXXKNKG-----
chicken.GBP	48	YRTGKSFLMNRLAQKRTGFPLGPTVYAEETKGIWMWCQPHPRQPRVTLVLL
GBP-4	47	YRTGKSYLMNKLAKGKNGFSVASTVQSHTKGIWICVPHPNWPNTLVLL
mouse.purine.nuc.BP	91	DTEGLGDEVKGDPKNDSWIFALAMLLSSTFVYNSMSTINQOALEQLHFVT
mu.GBP1	97	DTEGLEDVEKGDNQNDCWIFALAVLLSSTFVYNSMGTINQOAMDQQLHYVT
rat.GBP.p67	99	DTEGLEDVEKGDNQNDCWIFALAVLLSSTFVYNSMGTINQOAMDQQLHYVT
pig.GBP-1.partial	99	GT-----
chicken.GBP	96	DTEGLEDPNKNDNDHSDAWIFIALLLSSTFVYNSVGTIDORALS---SC
GBP-4	97	DTEGLGDEVKAQDNKNDIQIFALALLSSTFVYNTVNKIDQGAIDLHLHNT
mouse.purine.nuc.BP	141	ELTDQIRAKSSPREDKVKDSSEFVGFFPDFIIVAVRDFALEELKLNGRPIE
mu.GBP1	147	ELTDQIISKSSSPDQSDVDSANFVGFFPIFVWTLRDFSLDLEFDGESITP
rat.GBP.p67	149	ELTDQIISKSSSPDQSGIDDSANFVGFFPTFVWALRDFSLLEVNNGKLVTP
chicken.GBP	144	AGNGAVRAHPRGEKDN-NPASNFVSIIFPGFVWTVRDFTLQQLRGEKTLSE
GBP-4	147	ELTDQIILKARNSPDLDRVEDPADSASFFPDIVWTLRDFCLGLEIDGQLVTP
mouse.purine.nuc.BP	191	DEYLENALKLIOQGDNLKVQQSNMTRCTIRYFFPVRKCFMFDRTSDKRLI
mu.GBP1	197	DEYLELTSIALLRKGTDENTKKFNMPPRLCIRKFFPKRKCFIFDRPGDRKQ-L
rat.GBP.p67	199	DEYLEHSLTLKKGADKKTFSNEPRLCIRKFFPKRKCFIFDRPALRKQ-L
chicken.GBP	193	DEYLEDVLRURPGAGRRQERNELRR-CLPNFFFPRKLFITMERPAADAN-L
GBP-4	197	DEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKCFIFDLPQAHQKK-L
mouse.purine.nuc.BP	241	LQIENVPENQIERNQVESEKFCSYIFTNGKTTLRGGIVITGNRLGTLV
mu.GBP1	246	SKLEWIOEDQDLNKEFVEQVAEFTSYIFSYSGVKTLSSGGITVNGPRLKSLV
rat.GBP.p67	248	CKLETLGEEELCSEFVEQVAEFTSYIFSYSAVKTLSSGGIIVNGPRLKSLV
chicken.GBP	241	TRLEELRDEDELQPGFRKQVDAFCRYIWEAPVKVLPGGHOVTGSAALAYLV
GBP-4	246	AQLETLPDDELEPEEVQOVTETFCSYIFSHSMTKTLPPGGIMVNGSRLKNLV
mouse.purine.nuc.BP	291	QTYVNAISNSGTVPCLENAVTTLAQRENSIAVQKAADHYSEOMAORMRLPT
mu.GBP1	296	QTYVSAICSGELPCMENAVTLAQIENSAAVQKAITYYEEQMINOKIHMPT
rat.GBP.p67	298	QTYVGAISSGSLPCMESAVALTLAQIENSAAVQKAITHYEEQMINOKIQMPT
chicken.GBP	291	EKYMAAISSGSVPVCVESTLKALAOAENIAAVQMAVAEYORGMEOGLVLPT
GBP-4	296	LTYVNAISSGDLPCLENAVLALAQRENSAAVQKAIAHYDOQMGOKVOLPM
mouse.purine.nuc.BP	341	DTLQELLTVHAACEKEAIAVFMEMHSFKDDEQEFQKKLUVTIEERKEFIR
mu.GBP1	346	ETLQELLLDLHRTCEREAIEVFMKNSFKDVDQKFQEEELGAOLEAKRDAFK
rat.GBP.p67	348	ETLQELLLDLHRLIEREAEIEIFLKNSSFKDVDQKFQEEELCNLLISKRDAFIK
chicken.GBP	341	ASYDALLAVHRDCEQRALALFLSRAFADHKHOYHDELVHLEGQRGVLP
GBP-4	346	ETLQELLLDLHRTSEREAEIEVFMKNSSFKDVDQSFQKELETILDAKQNDICK
mouse.purine.nuc.BP	391	QNEAASIRHQAELERLSESIRKSISCGAFSVPGGHSLYLEARKKIELGY
mu.GBP1	396	KNMDMSSAHCSDLLEGFAHLEEEVKQGTFYKPGGYYLFLQRKQELEKKY
rat.GBP.p67	398	KNSDVSSAHCSDLIEDIFGPLEEVEVKQGTFSKPGGFLFLQMRQELEKKY
chicken.GBP	391	QQGGVGAAPVHGAAGAVEGR-GRRLQRGDYVARGGAQLFKEDVNRVLEEY
GBP-4	396	RNLEASSDYSALLKDFFGPLEEAVKQGIYSKPGGHNLFIQKTEELKAKY

FIG. 3A

mouse.purine.nuc.BP	441	Q[Q]VLRKGLK[A]KE[V]LKSFLQ[S]PAIMEDS[Q]QSDKALT[D]GERAIAAAERT[K]K
mu.GBP1	446	I[Q]TPGKGLQAE[V]MLRKYFES[K]EDLADTLLKMDQSLTEKEKQIEMERIKAE
rat.GBP.p67	448	N[Q]APGKGLEA[E]AVLKKYFES[K]EDIVETLLKTDQSLTEAAKEIEVERIKAE
pig.GBP-1.partial	101	-----PRG-----
chicken.GBP	440	K[Q]RPDKGVRAEAVLKEFLREH[E]GLAQVLKATEVQ[Q]ELAERQQEAAAEEAE
GBP-4	446	Y[Q]EPRKGIQAE[V]LQYLK[S]KEVSHAI[Q]TDQALTEKKKEAQVKAE
mouse.purine.nuc.BP	491	V[A]EKELEL[Q]RQ[K]E[Q]FQVMEAQ[E]RSFRENIAK[Q]EKMES---EKEMLLR
mu.GBP1	496	A[Q]EAANRALAEMQK[K]HEMLMEQ[K]E[Q]SYQEHMKQ[Q]LTEKMEQ---ERKELMA
rat.GBP.p67	498	T[A]EAANRELAEKQ[E]K[F]E[L]MMQQKE[E]SYQEHVRQ[Q]LTEKMK[E]---EQKKLIE
chicken.GBP	490	A[A]RKATEAWREDQ[K]-----RSMEEH[K]Q[Q]LEQWMKK---EKHTWEE
GBP-4	496	A[E]KAEAQR[Q]AAI[Q]RQN[E]QMMQER[E]RLHQ[E]QVRQ[Q]MEIAKQNWLAEQQKMQE
mouse.purine.nuc.BP	538	E[Q]EKMLEHKLKVQEEL[Q]IEG[F]REKSDMLKNE[Q]SHLREEMERTRRKPSLFG
mu.GBP1	543	E[Q]QRIISLKLQEQERLLKQGFQNESLQLRQE[Q]IEKIK-NMPPPRS-----
rat.GBP.p67	545	E[Q]DNIIIAKLRLREQEKF[Q]REGYENESKKLLRE[Q]IENMK-RRQSPGK-----
chicken.GBP	527	E[L]NRMLEHHRKEYKALLQEGFRREAAAKEKQ[Q]IRELQEEMRSCN-----
GBP-4	546	Q[Q]MQVFINCFFISPLPVTCVSSGKEGEAARSCGSQ-QGVWSQK-----
mouse.purine.nuc.BP	588	QILD TIGNAFIMI[Q]PGAGKLFVGVLKFLGSLSS
mu.GBP1	586	-----CTIL-----
rat.GBP.p67	588	-----CTIL-----
chicken.GBP	570	-----CTVL-----
GBP-4	589	-----VWV-----

FIG. 3B

hGBP-4								
67		hGBP-1						
64		76	hGBP-2					
60		68	71	rGBP				
59		70	71	80	mGBP-1			
49		54	54	52	53	mPNBP		
37		41	41	41	39	41	cGBP	

FIG. 4

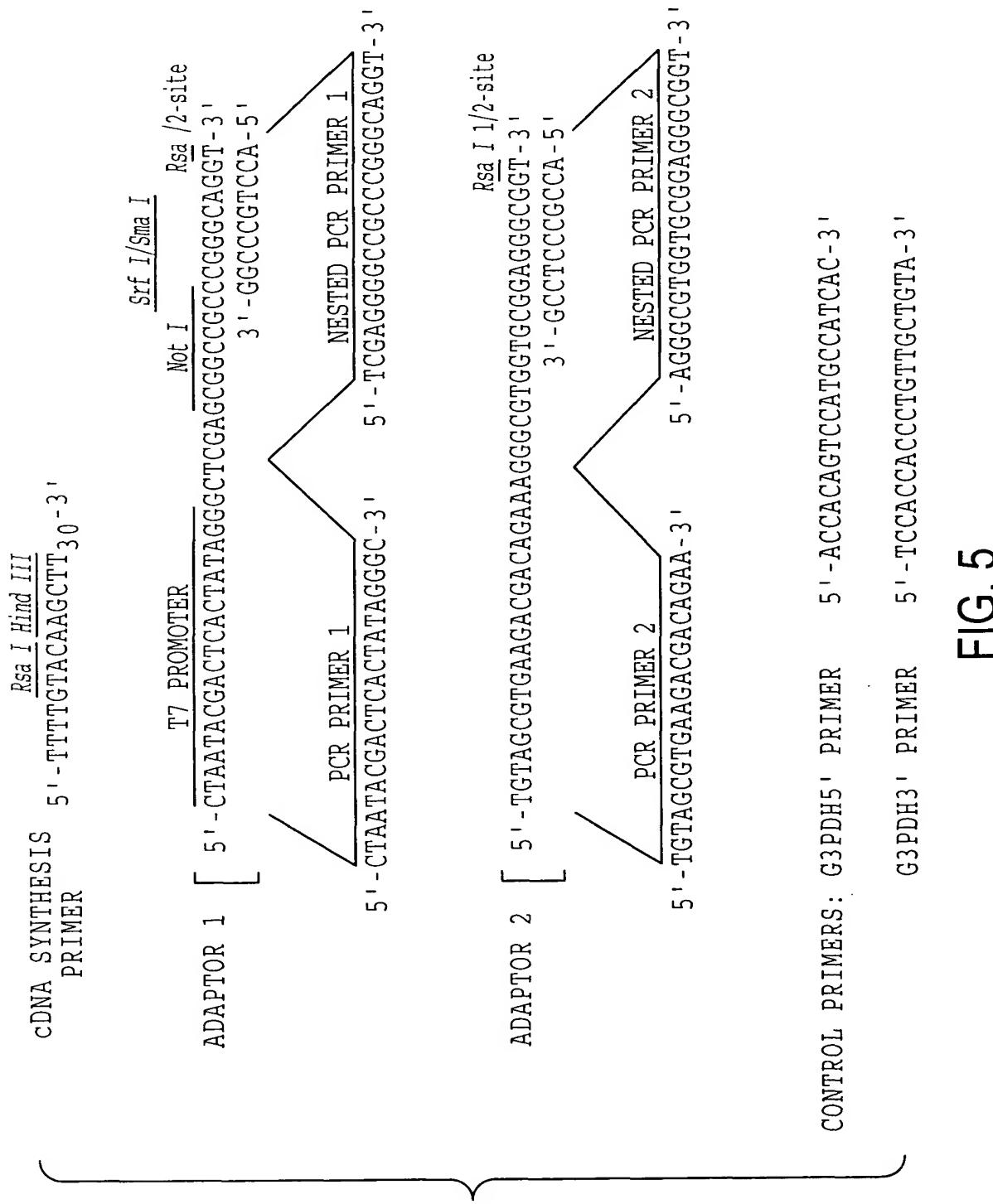


FIG. 5

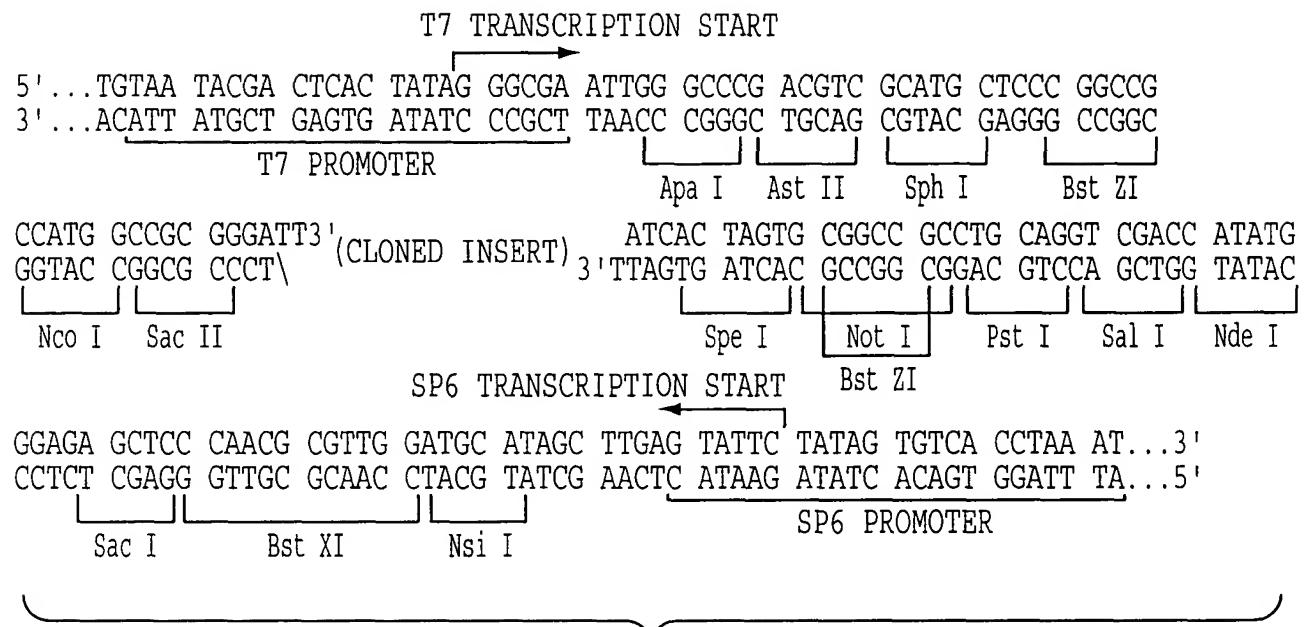


FIG. 6

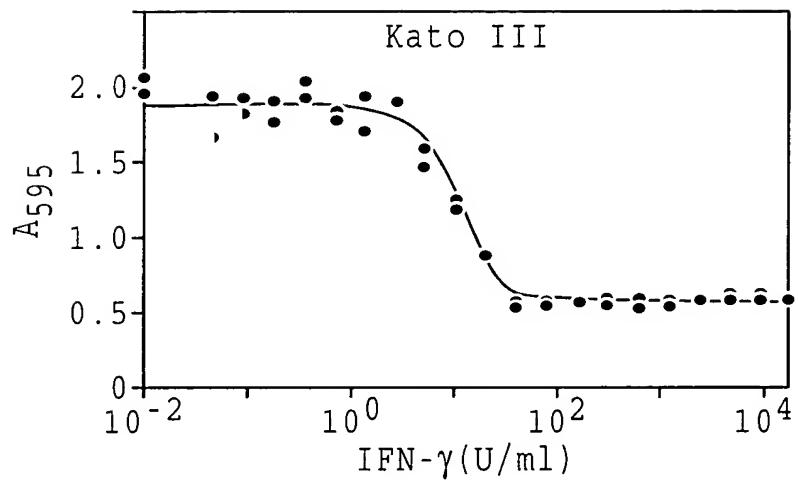


FIG. 7A

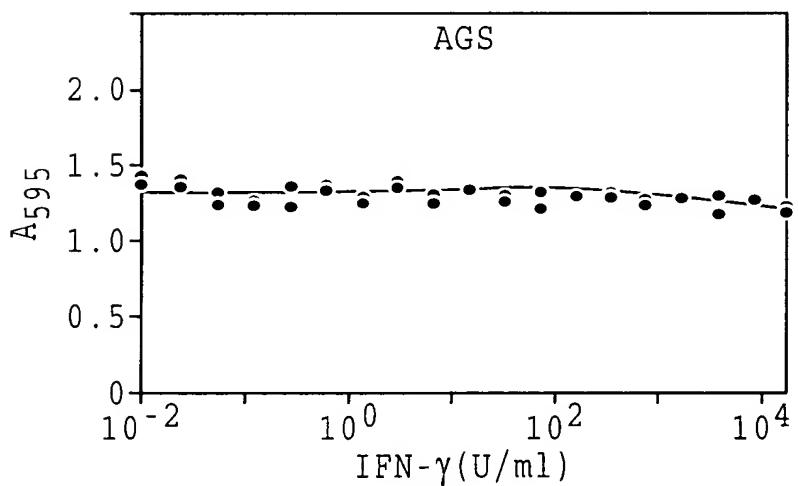


FIG. 7B

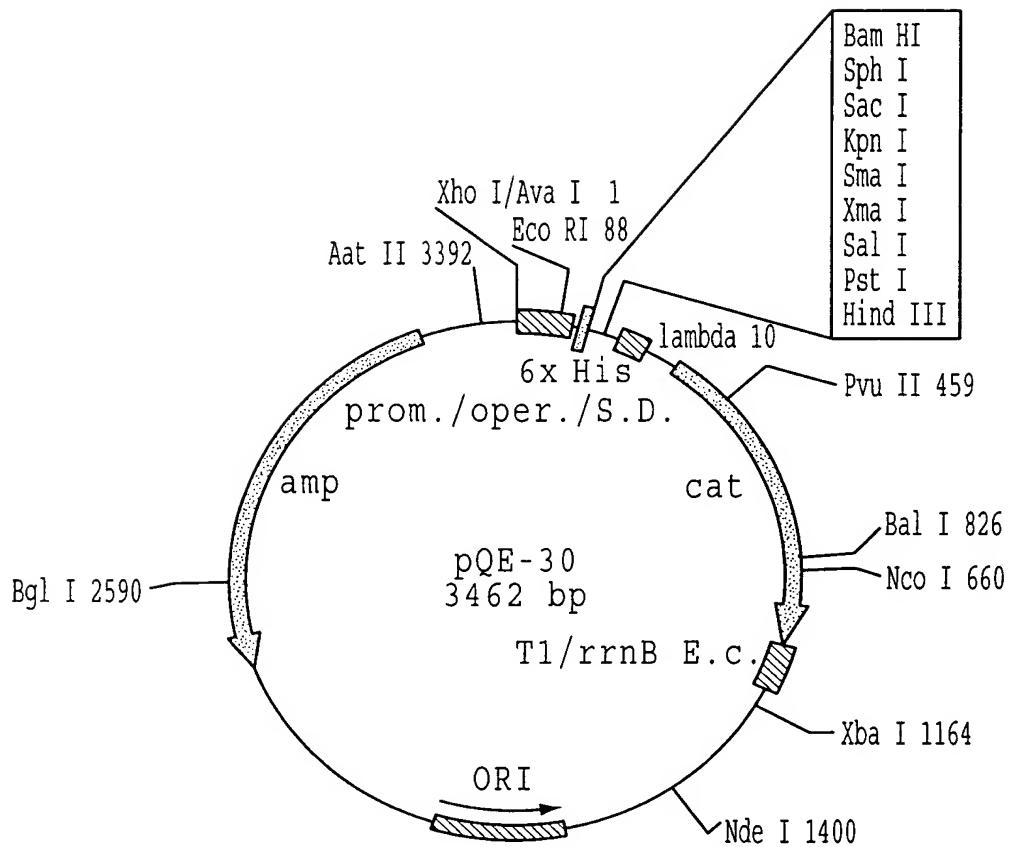


FIG. 8